GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: May 4, 2006, 08:03:10 ; Search time 187 Seconds
(without alignments)
662.593 Million cell updates/sec

Title: US-09-904-532B-127
Perfect score: 1503
Sequence: 1 MSGGWMAQVGAWRTGALGLA.....GLLVAMKESLLLSEQKTSLP 282

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1503	100.0	282	2	AAY13365	Aay13365 Amino aci
2	1503	100.0	282	2	AAY32926	Aay32926 Transmemb
3	1503	100.0	282	3	AAB24398	Aab24398 Human PRO
4	1503	100.0	282	3	AAY95342	Aay95342 Human PRO
5	1503	100.0	282	3	AAY97290	Aay97290 Lipid ass
6	1503	100.0	282	3	ADC78447	Adc78447 Human PRO
7	1503	100.0	282	4	AAB80233	Aab80233 Human PRO
8	1503	100.0	282	4	AAU12327	Aau12327 Human PRO
9	1503	100.0	282	4	AAB53079	Aab53079 Human ang
10	1503	100.0	282	4	AAM38847	Aam38847 Human pol
11	1503	100.0	282	4	ABU52728	Abu52728 Human met
12	1503	100.0	282	5	ABB90364	Abb90364 Human pol
13	1503	100.0	282	6	ABU71611	Abu71611 Human PRO
14	1503	100.0	282	6	ABO17771	Abo17771 Novel hum
15	1503	100.0	282	6	ABU71466	Abu71466 Human PRO
16	1503	100.0	282	6	ABJ37041	Abj37041 Human bre
17	1503	100.0	282	6	ABU81025	Abu81025 Human PRO
18	1503	100.0	282	6	ABU71912	Abu71912 Human sec
19	1503	100.0	282	6	ABO01795	Abo01795 Novel hum
20	1503	100.0	282	6	ABU66725	Abu66725 Human PRO
21	1503	100.0	282	6	ABU54368	Abu54368 Human sec
22	1503	100.0	282	6	ABO47383	Abo47383 Human sec
23	1503	100.0	282	6	ABU59806	Abu59806 Novel sec
24	1503	100.0	282	6	ABO24996	Abo24996 Human sec
25	1503	100.0	282	6	ABU64520	Abu64520 Human sec
26	1503	100.0	282	6	ABU67366	Abu67366 Human sec
27	1503	100.0	282	6	ABO14886	Abo14886 Human sec
28	1503	100.0	282	6	ABU67001	Abu67001 Human sec
29	1503	100.0	282	6	ABU69643	Abu69643 Novel hum
30	1503	100.0	282	6	ABO14825	Abo14825 Human sec
31	1503	100.0	282	6	ADA45831	Ada45831 Novel hum
32	1503	100.0	282	6	ADA76262	Ada76262 Human PRO
33	1503	100.0	282	6	ADB29332	Adb29332 Human sec
34	1503	100.0	282	6	ADA18912	Ada18912 Human PRO
35	1503	100.0	282	6	ADA61535	Ada61535 Homo sapi
36	1503	100.0	282	6	ADB19320	Adb19320 Novel hum
37	1503	100.0	282	6	ADB27861	Adb27861 Human PRO
38	1503	100.0	282	6	ADA86340	Ada86340 Novel hum
39	1503	100.0	282	6	ADB15904	Adb15904 Human PRO
40	1503	100.0	282	6	ADA47690	Ada47690 Human PRO
41	1503	100.0	282	6	ADA18188	Ada18188 Human sec
42	1503	100.0	282	6	ABO32777	Abo32777 Human sec
43	1503	100.0	282	6	ADA67485	Ada67485 Human PRO
44	1503	100.0	282	6	ADB30492	Adb30492 Human PRO
45	1503	100.0	282	6	ADA85788	Ada85788 Novel hum
46	1503	100.0	282	6	ADA97000	Ada97000 Human PRO
47	1503	100.0	282	6	ADA79304	Ada79304 Human PRO
48	1503	100.0	282	6	ADA87443	Ada87443 Novel hum
49	1503	100.0	282	6	ADB16645	Adb16645 Human PRO
50	1503	100.0	282	6	ABO34837	Abo34837 Human PRO
51	1503	100.0	282	6	ADA16163	Ada16163 Human sec
52	1503	100.0	282	6	ADA91737	Ada91737 Novel hum
53	1503	100.0	282	6	ADB14800	Adb14800 Human PRO
54	1503	100.0	282	6	ADB18761	Adb18761 Novel hum
55	1503	100.0	282	6	ADA93976	Ada93976 Human PRO
56	1503	100.0	282	6	ADB19872	Adb19872 Novel hum
57	1503	100.0	282	6	ADB13184	Adb13184 Human PRO
58	1503	100.0	282	6	ABO43304	Abo43304 Novel hum
59	1503	100.0	282	6	ADA74438	Ada74438 Human PRO
60	1503	100.0	282	6	ADA42308	Ada42308 Human sec
61	1503	100.0	282	6	ADB24671	Adb24671 Human PRO
62	1503	100.0	282	6	ADA82195	Ada82195 Human PRO
63	1503	100.0	282	6	ADA75158	Ada75158 Human PRO
64	1503	100.0	282	6	ADA85236	Ada85236 Novel hum
65	1503	100.0	282	6	ADA84684	Ada84684 Novel hum
66	1503	100.0	282	6	ABO17515	Abo17515 Human PRO
67	1503	100.0	282	6	ADB29940	Adb29940 Human PRO
68	1503	100.0	282	6	ADA80468	Ada80468 Human PRO
69	1503	100.0	282	6	ADA75710	Ada75710 Human PRO
70	1503	100.0	282	6	ADA46935	Ada46935 Human PRO
71	1503	100.0	282	6	ADB25231	Adb25231 Human PRO
72	1503	100.0	282	6	ADA93407	Ada93407 Human PRO
73	1503	100.0	282	6	ADB26757	Adb26757 Human PRO
74	1503	100.0	282	6	ADB31044	Adb31044 Human PRO
75	1503	100.0	282	6	ADA60972	Ada60972 Homo sapi
76	1503	100.0	282	6	ADB24119	Adb24119 Human PRO
77	1503	100.0	282	6	ADA96448	Ada96448 Human PRO
78	1503	100.0	282	6	ADA81020	Ada81020 Human PRO
79	1503	100.0	282	6	ADA95896	Ada95896 Human PRO
80	1503	100.0	282	6	ADB26205	Adb26205 Human PRO
81	1503	100.0	282	6	ADB21690	Adb21690 Novel hum
82	1503	100.0	282	7	ADA77469	Ada77469 Human PRO
83	1503	100.0	282	7	ADB18209	Adb18209 Human PRO
84	1503	100.0	282	7	ADA86892	Ada86892 Novel hum
85	1503	100.0	282	7	ADA16587	Ada16587 Human sec
86	1503	100.0	282	7	ADA13016	Ada13016 Human sec
87	1503	100.0	282	7	ADA41884	Ada41884 Human sec
88	1503	100.0	282	7	ADA87995	Ada87995 Novel hum
89	1503	100.0	282	7	ADA46383	Ada46383 Novel hum
90	1503	100.0	282	7	ADA17231	Ada17231 Human sec
91	1503	100.0	282	7	ADA42734	Ada42734 Human sec
92	1503	100.0	282	7	ADB28413	Adb28413 Human PRO
93	1503	100.0	282	7	ADB28965	Adb28965 Human PRO
94	1503	100.0	282	7	ADA76917	Ada76917 Human PRO
95	1503	100.0	282	7	ADA88547	Ada88547 Novel hum
96	1503	100.0	282	7	ADA97552	Ada97552 Human PRO
97	1503	100.0	282	7	ADB27309	Adb27309 Human PRO

98	1503	100.0	282	7	ADB22242	Adb22242	Novel	hum	171	1503	100.0	282	7	ADE03956	Ade03956 Human PRO
99	1503	100.0	282	7	ABO17576	Abo17576	Human	PRO	172	1503	100.0	282	7	ADE32253	Ade32253 Novel hum
100	1503	100.0	282	7	ADA66933	Ada66933	Human	PRO	173	1503	100.0	282	7	ADE22185	Ade22185 Human PRO
101	1503	100.0	282	7	ADB22794	Adb22794	Human	PRO	174	1503	100.0	282	7	ADD79409	Add79409 Human PRO
102	1503	100.0	282	7	ADB23567	Adb23567	Human	PRO	175	1503	100.0	282	7	ADE41945	Ade41945 Human PRO
103	1503	100.0	282	7	ADA92289	Ada92289	Novel	hum	176	1503	100.0	282	7	ADE17762	Ade17762 Human PRO
104	1503	100.0	282	7	ADB15352	Adb15352	Human	PRO	177	1503	100.0	282	7	ADD91894	Add91894 Human PRO
105	1503	100.0	282	7	ADB38604	Adb38604	Novel	hum	178	1503	100.0	282	7	ADE33357	Ade33357 Novel hum
106	1503	100.0	282	7	ADB38052	Adb38052	Novel	hum	179	1503	100.0	282	7	ADE33909	Ade33909 Novel hum
107	1503	100.0	282	7	ADB66524	Adb66524	Novel	hum	180	1503	100.0	282	7	ADD79961	Add79961 Human PRO
108	1503	100.0	282	7	ADB89604	Adb89604	Human	PRO	181	1503	100.0	282	7	ADD92998	Add92998 Human PRO
109	1503	100.0	282	7	ADB90336	Adb90336	Human	PRO	182	1503	100.0	282	7	ADE19418	Ade19418 Human PRO
110	1503	100.0	282	7	ADB77653	Adb77653	Human	sec	183	1503	100.0	282	7	ADE34760	Ade34760 Human sec
111	1503	100.0	282	7	ADB39437	Adb39437	Novel	hum	184	1503	100.0	282	7	ADE18866	Ade18866 Human PRO
112	1503	100.0	282	7	ADB74789	Adb74789	Human	sec	185	1503	100.0	282	7	ADE43062	Ade43062 Human PRO
113	1503	100.0	282	7	ADB47060	Adb47060	Novel	hum	186	1503	100.0	282	7	ADD95851	Add95851 Human PRO
114	1503	100.0	282	7	ADB86667	Adb86667	Human	PRO	187	1503	100.0	282	7	ADE22737	Ade22737 Human PRO
115	1503	100.0	282	7	ADB77272	Adb77272	Novel	hum	188	1503	100.0	282	7	ADD78855	Add78855 Human PRO
116	1503	100.0	282	7	ADB34429	Adb34429	Human	PRO	189	1503	100.0	282	7	ADE32805	Ade32805 Novel hum
117	1503	100.0	282	7	ADB35533	Adb35533	Human	PRO	190	1503	100.0	282	7	ADE42497	Ade42497 Human PRO
118	1503	100.0	282	7	ADB33877	Adb33877	Human	PRO	191	1503	100.0	282	7	ADD80513	Add80513 Human PRO
119	1503	100.0	282	7	ADB34981	Adb34981	Human	PRO	192	1503	100.0	282	7	ADD89541	Add89541 Human PRO
120	1503	100.0	282	7	ADB36085	Adb36085	Human	PRO	193	1503	100.0	282	7	ADE40825	Ade40825 Human PRO
121	1503	100.0	282	7	ADB46480	Adb46480	Novel	hum	194	1503	100.0	282	7	ADE04624	Ade04624 Human PRO
122	1503	100.0	282	7	ADC28435	Adc28435	Human	sec	195	1503	100.0	282	7	ADE92753	Ade92753 Human PRO
123	1503	100.0	282	7	ADC39635	Adc39635	Human	sec	196	1503	100.0	282	7	ADG21462	Adg21462 Novel hum
124	1503	100.0	282	7	ADC40149	Adc40149	Human	sec	197	1503	100.0	282	7	ADF77329	Adf77329 Human 8D6
125	1503	100.0	282	7	ADC18977	Adc18977	Human	sec	198	1503	100.0	282	7	ADG23103	Adg23103 Novel hum
126	1503	100.0	282	7	ADC34273	Adc34273	Human	sec	199	1503	100.0	282	7	ADF97438	Adf97438 Human PRO
127	1503	100.0	282	7	ADC29328	Adc29328	Human	sec	200	1503	100.0	282	7	ADG10648	Adg10648 Human STA
128	1503	100.0	282	7	ADC28859	Adc28859	Human	sec	201	1503	100.0	282	7	ADG80502	Adg80502 Human PRO
129	1503	100.0	282	7	ADC40744	Adc40744	Human	sec	202	1503	100.0	282	7	ADG79950	Adg79950 Human PRO
130	1503	100.0	282	7	ADC19401	Adc19401	Human	sec	203	1503	100.0	282	7	ADH59243	Adh59243 Human sec
131	1503	100.0	282	7	ADC33849	Adc33849	Human	sec	204	1503	100.0	282	7	ADH55242	Adh55242 Novel hum
132	1503	100.0	282	7	ADC12919	Adc12919	Human	sec	205	1503	100.0	282	7	ADH55794	Adh55794 Novel hum
133	1503	100.0	282	7	ADC50353	Adc50353	Novel	hum	206	1503	100.0	282	7	ADI38022	Adi38022 Human sec
134	1503	100.0	282	7	ADC71900	Adc71900	Novel	hum	207	1503	100.0	282	7	ADI64962	Adi64962 Novel hum
135	1503	100.0	282	7	ADC59879	Adc59879	Novel	hum	208	1503	100.0	282	7	ADI63461	Adi63461 Novel hum
136	1503	100.0	282	7	ADC52886	Adc52886	Novel	hum	209	1503	100.0	282	7	ADH81875	Adh81875 Novel hum
137	1503	100.0	282	7	ADC57240	Adc57240	Novel	hum	210	1503	100.0	282	7	ADH81323	Adh81323 Novel hum
138	1503	100.0	282	7	ADC60431	Adc60431	Novel	hum	211	1503	100.0	282	7	ADJ26290	Adj26290 Human sec
139	1503	100.0	282	7	ADC50906	Adc50906	Novel	hum	212	1503	100.0	282	7	ADM82492	Adm82492 Novel hum
140	1503	100.0	282	7	ADC65433	Adc65433	Human	PRO	213	1503	100.0	282	7	ADN15891	Adn15891 Novel hum
141	1503	100.0	282	7	ADC54531	Adc54531	Novel	hum	214	1503	100.0	282	7	ADN16520	Adn16520 Novel hum
142	1503	100.0	282	7	ADC53492	Adc53492	Novel	hum	215	1503	100.0	282	7	ADN15339	Adn15339 Novel hum
143	1503	100.0	282	7	ADC59015	Adc59015	Novel	hum	216	1503	100.0	282	7	ADN14787	Adn14787 Novel hum
144	1503	100.0	282	7	ADC55893	Adc55893	Novel	hum	217	1503	100.0	282	7	ADI64013	Adi64013 Novel hum
145	1503	100.0	282	7	ADC58463	Adc58463	Novel	hum	218	1503	100.0	282	8	ADC81049	Adc81049 Novel hum
146	1503	100.0	282	7	ADC12371	Adc12371	Human	sec	219	1503	100.0	282	8	ADE79205	Ade79205 Human sec
147	1503	100.0	282	7	ADD03137	Add03137	Novel	hum	220	1503	100.0	282	8	ADD76497	Add76497 Human PRO
148	1503	100.0	282	7	ADC90129	Adc90129	Novel	hum	221	1503	100.0	282	8	ADD87861	Add87861 Human PRO
149	1503	100.0	282	7	ADC69548	Adc69548	Human	PRO	222	1503	100.0	282	8	ADD86265	Add86265 Human PRO
150	1503	100.0	282	7	ADC48437	Adc48437	Human	PRO	223	1503	100.0	282	8	ADE79629	Ade79629 Human sec
151	1503	100.0	282	7	ADD09966	Add09966	Human	PRO	224	1503	100.0	282	8	ADE75713	Ade75713 Human PRO
152	1503	100.0	282	7	ADD04541	Add04541	Novel	hum	225	1503	100.0	282	8	ADE73305	Ade73305 Human sec
153	1503	100.0	282	7	ADC80497	Adc80497	Novel	hum	226	1503	100.0	282	8	ADE23289	Ade23289 Human PRO
154	1503	100.0	282	7	ADD11004	Add11004	Human	PRO	227	1503	100.0	282	8	ADE23841	Ade23841 Human PRO
155	1503	100.0	282	7	ADC47885	Adc47885	Human	PRO	228	1503	100.0	282	8	ADE24484	Ade24484 Human PRO
156	1503	100.0	282	7	ADD04926	Add04926	Human	sec	229	1503	100.0	282	8	ADD87309	Add87309 Human PRO
157	1503	100.0	282	7	ADC79945	Adc79945	Novel	hum	230	1503	100.0	282	8	ADE89175	Ade89175 Human PRO
158	1503	100.0	282	7	ADD09414	Add09414	Human	PRO	231	1503	100.0	282	8	ADE73840	Ade73840 Human sec
159	1503	100.0	282	7	ADD03932	Add03932	Human	sec	232	1503	100.0	282	8	ADE18314	Ade18314 Human PRO
160	1503	100.0	282	7	ADD03508	Add03508	Human	sec	233	1503	100.0	282	8	ADE88623	Ade88623 Human PRO
161	1503	100.0	282	7	ADD41127	Add41127	Novel	hum	234	1503	100.0	282	8	ADE99394	Ade99394 Human sec
162	1503	100.0	282	7	ADD52266	Add52266	Human	PRO	235	1503	100.0	282	8	ADE94643	Ade94643 Human PRO
163	1503	100.0	282	7	ADD53006	Add53006	Human	PRO	236	1503	100.0	282	8	ADE91054	Ade91054 Human PRO
164	1503	100.0	282	7	ADD53558	Add53558	Novel	hum	237	1503	100.0	282	8	ADE95195	Ade95195 Human PRO
165	1503	100.0	282	7	ADD51714	Add51714	Human	PRO	238	1503	100.0	282	8	ADE93305	Ade93305 Human PRO
166	1503	100.0	282	7	ADD02513	Add02513	Human	PRO	239	1503	100.0	282	8	ADF34886	Adf34886 Human PRO
167	1503	100.0	282	7	ADD01947	Add01947	Human	PRO	240	1503	100.0	282	8	ADE98513	Ade98513 Human sec
168	1503	100.0	282	7	ADD54129	Add54129	Novel	hum	241	1503	100.0	282	8	ADE92201	Ade92201 Novel hum
169	1503	100.0	282	7	ADD92446	Add92446	Human	PRO	242	1503	100.0	282	8	ADE90502	Ade90502 Human PRO
170	1503	100.0	282	7	ADD91342	Add91342	Human	PRO	243	1503	100.0	282	8	ADE91649	Ade91649 Novel hum

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: May 1, 2006, 17:51:56 ; Search time 40 Seconds
(without alignments)
678.328 Million cell updates/sec

Title: US-09-904-532B-127
Perfect score: 1503
Sequence: 1 MSGGWMAQVGAWRTGALGLA.....GLLVAMKESLLLSEQKTSLP 282

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	293.5	19.5	996	2	JE0237	apolipoprotein E r
2	286.5	19.1	863	1	S51789	VLDL receptor prec
3	280.5	18.7	873	1	A49729	VLDL receptor prec
4	278.5	18.5	869	1	JC4858	VLDL receptor prec
5	275	18.3	873	1	I48952	VLDL receptor prec
6	268	17.8	873	1	QRRBVD	VLDL receptor prec
7	259	17.2	972	2	A30363	glycoprotein GP330
8	255.5	17.0	4660	2	T42737	gp330 protein prec
9	251	16.7	4544	1	S02392	alpha-2-macroglobu
10	251	16.7	4545	1	S25111	alpha-2-macroglobu
11	250	16.6	4543	1	A53102	alpha-2-macroglobu
12	245.5	16.3	4753	1	A47437	LDL-receptor-relat
13	244	16.2	1984	2	T13171	probable vitelloge
14	239	15.9	2215	2	T00348	LR11 protein - mou
15	237.5	15.8	2180	2	T29764	hypothetical prote
16	234	15.6	1357	2	T16860	hypothetical prote
17	234	15.6	1650	2	S53457	dominant autoantig
18	229	15.2	1142	2	T30272	hypothetical prote
19	227	15.1	4391	2	A38096	perlecan precursor
20	226.5	15.1	860	1	QRHULD	LDL receptor precu
21	226	15.0	837	1	A29512	LDL receptor precu
22	223.5	14.9	909	1	QRXLL1	LDL receptor 1 pre
23	223.5	14.9	909	1	QRXLL2	LDL receptor 2 pre
24	223.5	14.9	1615	2	JE0372	low density lipopr
25	222.5	14.8	925	2	T37475	lipoprotein recept
26	219.5	14.6	621	2	I38467	low density lipopr
27	216	14.4	1113	2	JE0315	low-density lipopr
28	216	14.4	3707	2	S18252	heparan sulfate pr
29	215.5	14.3	527	2	JE0373	low density lipopr
30	215.5	14.3	862	1	QRMSLD	LDL receptor precu
31	214.5	14.3	1661	2	T31330	head-activator bin
32	214	14.2	854	1	QRHYLD	LDL receptor precu
33	214	14.2	1613	2	JE0272	low density lipopr
34	214	14.2	1613	2	JE0273	low density lipopr
35	208	13.8	2616	2	A57096	nudel protein prec
36	207	13.8	879	1	QRRTLD	LDL receptor precu
37	205	13.6	1847	2	T18308	probable vitelloge
38	202.5	13.5	548	2	T16642	hypothetical prote
39	196.5	13.1	1297	2	T30274	proteoliaisin - se
40	193.5	12.9	855	2	JC7731	membrane-bound arg
41	191.5	12.7	574	2	B88465	protein B0244.8 [i
42	184.5	12.3	770	2	T00203	LDL receptor-relat
43	183.5	12.2	770	2	T00204	LDL receptor relat
44	183	12.2	1160	2	F88369	protein unc-52 [im
45	183	12.2	2295	2	C88369	protein unc-52 [im
46	183	12.2	3375	2	T19821	hypothetical prote
47	182	12.1	1115	2	S40241	G protein-coupled
48	181.5	12.1	2643	2	T29149	hypothetical prote
49	168	11.2	905	2	T23229	hypothetical prote
50	165.5	11.0	250	2	T30124	hypothetical prote
51	160.5	10.7	198	2	T24476	hypothetical prote
52	160.5	10.7	435	2	I54182	tumor necrosis fac
53	160	10.6	1609	2	S44821	F44E2.4 protein -
54	156.5	10.4	394	2	T20633	hypothetical prote
55	141	9.4	531	2	T18741	hypothetical prote
56	140.5	9.3	277	2	I37552	OX40 homolog - hum
57	137.5	9.1	157	2	B48837	subgroup A Rous sa
58	131.5	8.7	686	2	S43562	K08E5.3 protein -
59	131.5	8.7	752	2	T20871	hypothetical prote
60	131	8.7	354	2	T22274	hypothetical prote
61	130.5	8.7	120	2	A48837	subgroup A Rous sa
62	130.5	8.7	4006	2	T09070	probable tenascin
63	130	8.6	577	2	A60501	thrombomodulin pre
64	128.5	8.5	990	2	H88733	protein F32E10.3 [
65	127	8.4	1101	2	T16840	hypothetical prote
66	125	8.3	738	2	S40992	hypothetical prote
67	125	8.3	739	2	B88553	protein K04H4.2b [
68	124	8.3	308	2	JC7125	epidermal growth f
69	124	8.3	765	2	T35719	chitinase - Strept
70	124	8.3	1119	2	T16720	hypothetical prote
71	123.5	8.2	3133	2	S52093	hemocytin - silkwo
72	122.5	8.2	427	1	GQHUN	nerve growth facto
73	122	8.1	3566	1	A40701	tenascin-X precurs
74	121.5	8.1	197	2	T10081	sperm mitochondria
75	120	8.0	1428	2	T08852	lustrin A - Califo
76	119	7.9	251	2	A55035	cysteine-rich prot
77	118.5	7.9	613	2	S15468	complement C3b/C4b
78	118	7.9	2120	2	T30243	alpha tectorin - c
79	117.5	7.8	558	2	T15448	hypothetical prote
80	117.5	7.8	4135	2	T42629	tenascin-X - bovin
81	114.5	7.6	356	2	A25918	thrombomodulin - b
82	113.5	7.6	1035	1	A43090	enteropeptidase (E
83	113	7.5	525	2	B48058	RNA-binding protei
84	113	7.5	546	2	JC4798	seizure-related me
85	112.5	7.5	591	2	I48141	acrogranin - guine
86	111	7.4	469	1	S29126	properdin precurso
87	111	7.4	1721	1	I38902	retinoblastoma bin
88	110.5	7.4	579	2	JC7629	membrane-type friz
89	110	7.3	1964	2	T09059	notch4 - mouse
90	109.5	7.3	1959	1	AGRT	agrin - rat
91	108.5	7.2	2524	2	A35844	Xotch protein - Af
92	108	7.2	316	2	G86333	hypothetical prote
93	108	7.2	1328	2	T43060	agrin - electric r
94	107.5	7.2	784	2	JQ0317	hypothetical 82K p
95	107.5	7.2	1746	1	S19694	tenascin precursor
96	107.5	7.2	1955	1	AGCH	agrin precursor -
97	107.5	7.2	2201	2	A32160	tenascin-C - human
98	107.5	7.2	2703	1	A24420	notch protein - fr
99	107.5	7.2	2824	2	T22759	hypothetical prote
100	107.5	7.2	2918	2	A54105	fibrillin-2 precur

ALIGNMENTS

RESULT 1
JE0237
apolipoprotein E receptor 2 precursor - mouse
N;Alternate names: apoER2
C;Species: Mus musculus (house mouse)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C;Accession: JE0237
R;Kim, H.J.; Kim, D.H.; Magoori, K.; Saeki, S.; Yamamoto, T.T.
J. Biochem. 124, 451-456, 1998
A;Title: Evolution of the apolipoprotein E receptor 2 gene by exon loss.
A;Reference number: JE0237; MUID:98352008; PMID:9685741
A;Accession: JE0237
A;Molecule type: mRNA
A;Residues: 1-996 <KIM>
A;Cross-references: UNIPROT:Q924X6; UNIPARC:UPI0000176758; DDBJ:D85463
C;Superfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homology;
C;Keywords: glycoprotein
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-996/Product: apolipoprotein E receptor 2 #status predicted <MAT>
F;41-75/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;80-116/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;121-157/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;161-195/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;200-237/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;251-286/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;291-325/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;331-368/Domain: LDL receptor ligand-binding repeat homology <LDL>
F;373-407/Domain: EGF homology <EGF>
F;585-628/Domain: LDL receptor YWTD-containing repeat homology <YWT>
F;723-767/Domain: EGF homology <EGF1>
F;858-881/Domain: transmembrane #status predicted <TTM>
F;805,840/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.5%; Score 293.5; DB 2; Length 996;
Best Local Similarity 40.2%; Pred. No. 2.4e-12;
Matches 68; Conservative 15; Mismatches 65; Indels 21; Gaps 7;

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Qy          8 QVGAWRTGALGLALLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSGLC 67
              ::|| |     |||||| | |   :|| ||      ||     |   :|:||    |
Db          5 ELGALRP----LALLLLLLLQLQHLSAADPL-----LGGQGPVK-ECEEDQFRCRNE-RC 53

Qy         68 VPLTWRCDRDLDCSDGSDEEECRIEPCT------QKGQCPPPPGLPCPCTGVSDCSGGTD 121
              :|| |||| | |||| |||::|    |         | | |       | |  :|  |:|
Db         54 IPLVWRCDEDNDCSDNSDEDDCPKRTCADSDFTCDNGHCIPE---RWKCDGEEECPDGSD 110

Qy        122 KKLRNCSRLACLAGELRC-TLSDDCIPLTWRCDGHPDCPDSSDELGCGT 169
              :    ||   | | :| |   |  |:| :|||||  ||   :|| || |
Db        111 ESKATCSSEECPAEKLSCGPTSHKCVPASWRCDGEKDCEGGADEAGCPT 159
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RESULT 2
S51789
VLDL receptor precursor - chicken
N;Alternate names: very low density lipoprotein receptor; vitellogenin receptor
C;Species: Gallus gallus (chicken)
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: S51789
R;Bujo, H.; Hermann, M.; Kaderli, M.O.; Jacobsen, L.; Sugawara, S.; Nimpf, J.; Yamamoto,
EMBO J. 13, 5165-5175, 1994
A;Title: Chicken oocyte growth is mediated by an eight ligand binding repeat member of t
A;Reference number: S51789; MUID:95045409; PMID:7957081
A;Accession: S51789
A;Molecule type: mRNA
A;Residues: 1-863 <BUJ>
A;Cross-references: UNIPROT:P98165; UNIPARC:UPI000011D6F0; EMBL:X80207; NID:g609265; PID
C;Comment: This receptor mediates uptake of very low density lipoprotein and vitellogeni
C;Comment: There is some evidence for the existence of a longer splice form containing a
C;Superfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homology;
C;Keywords: duplication; fatty acid metabolism; glycoprotein; receptor; transmembrane pr
F;1-44/Domain: signal sequence #status predicted <SIG>
F;45-863/Product: VLDL receptor #status predicted <MAT>
F;45-787/Domain: extracellular #status predicted <EXT>
F;51-85/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;90-126/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;131-167/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;172-206/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;211-247/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;257-291/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;296-330/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;336-373/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F;378-412/Domain: EGF homology <EG1>
F;418-452/Domain: EGF homology <EG2>
F;459-498/Domain: LDL receptor YWTD-containing repeat homology <YW1>
F;499-544/Domain: LDL receptor YWTD-containing repeat homology <YW2>
F;545-587/Domain: LDL receptor YWTD-containing repeat homology <YW3>
F;588-631/Domain: LDL receptor YWTD-containing repeat homology <YW4>
F;632-674/Domain: LDL receptor YWTD-containing repeat homology <YW5>
F;675-717/Domain: LDL receptor YWTD-containing repeat homology <YW6>
F;726-769/Domain: EGF homology <EG3>
F;788-809/Domain: transmembrane #status predicted <TMM>
F;824-828/Region: coated-pit mediated internalization signal
F;169,773/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;378-389,385-398,400-412,418-428,424-437,439-452,726-739,735-754,756-769/Disulfide

Query Match 19.1%; Score 286.5; DB 1; Length 863;
Best Local Similarity 38.4%; Pred. No. 6.2e-12;
Matches 63; Conservative 14; Mismatches 62; Indels 25; Gaps 7;

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Qy         12 WRTGALGLALLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSGLCVPLT 71
              |   | || ||| ||       | | |   |       |  ::||| ::| |:||
Db         23 WALPRCG-ALCLLLALGC--------LRTATDGAKA-----KCEESQFQC-SNGRCIPLL 67

Qy         72 WRCDRDLDCSDGSDEEECRIEPCTQ------KGQCPPPPGLPCPCTGVSDCSGGTDKKLR 125
              |:|| | ||||||||  |  : | :       ||| |       | |  ||  |:|:
Db         68 WKCDGDEDCSDGSDESACVKKTCAESDFVCNSGQCVPN---RWQCDGDPDCEDGSDESAE 124

Qy        126 NCSRLACLAGELRC-TLSDDCIPLTWRCDGHPDCPDSSDELGCG 168
              |   |  |: |   |  |||::|:|||  ||    ||  ||
Db        125 LCHMRTCRVNEISCGPQSTQCIPVSWKCDGEKDCDSGEDEENCG 168
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RESULT 3
A49729
VLDL receptor precursor, long splice form - human
N;Alternate names: very low density lipoprotein receptor; vitellogenin receptor
N;Contains: VLDL receptor short splice form
C;Species: Homo sapiens (man)
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: A49729; B49729; A54309; I54373; I59603
R;Sakai, J.; Hoshino, A.; Takahashi, S.; Miura, Y.; Ishii, H.; Suzuki, H.; Kawarabay
J. Biol. Chem. 269, 2173-2182, 1994
A;Title: Structure, chromosome location, and expression of the human very low densit
A;Reference number: A49729; MUID:94124575; PMID:8294473
A;Accession: A49729
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-873 <SAK>
A;Cross-references: UNIPROT:P98155; UNIPARC:UPI0000055935; GB:D16493; NID:g391733;
A;Accession: B49729
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-750,779-873 <SA2>
A;Cross-references: UNIPARC:UPI00001736CC; GB:D16494
R;Oka, K.; Tzung, K.W.; Sullivan, M.; Lindsay, E.; Baldini, A.; Chan, L.
Genomics 20, 298-300, 1994
A;Title: Human very-low-density lipoprotein receptor complementary DNA and deduced a
on.
A;Reference number: A54309; MUID:94292216; PMID:8020981
A;Accession: A54309
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12,'V',14-765,'S',767-873 <OKA>
A;Cross-references: UNIPARC:UPI000016B301; GB:L22431; NID:g437386; PIDN:AAA61344.1;

Thu May 4 07:04:18 2006

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: May 1, 2006, 17:48:35 ; Search time 230 Seconds
(without alignments)
865.039 Million cell updates/sec

Title: US-09-904-532B-127
Perfect score: 1503
Sequence: 1 MSGGWMAQVGAWRTGALGLA.....GLLVAMKESLLLSEQKTSLP 282

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1503	100.0	282	2	Q9NPF0_HUMAN	Q9npf0 homo sapien
2	1499	99.7	282	2	Q53HF7_HUMAN	Q53hf7 homo sapien
3	804.5	53.5	264	2	Q5HZW5_RAT	Q5hzw5 rattus norv
4	750.5	49.9	260	2	Q9Z1P5_MOUSE	Q9z1p5 m ng29 (put
5	744.5	49.5	260	2	Q9CWC2_MOUSE	Q9cwc2 mus musculu
6	742.5	49.4	260	2	Q8C2Q4_MOUSE	Q8c2q4 mus musculu
7	371	24.7	198	2	Q7TSW0_MOUSE	Q7tsw0 mus musculu
8	296.5	19.7	555	2	Q59HD7_HUMAN	Q59hd7 homo sapien
9	293.5	19.5	996	1	LRP8_MOUSE	Q924x6 mus musculu
10	286.5	19.1	863	1	VLDLR_CHICK	P98165 gallus gall
11	284.5	18.9	355	2	Q802V2_BRARE	Q802v2 brachydanio
12	280.5	18.7	700	2	Q5SW66_HUMAN	Q5sw66 homo sapien
13	280.5	18.7	845	2	Q5VVF5_HUMAN	Q5vvf5 homo sapien
14	280.5	18.7	873	1	VLDLR_HUMAN	P98155 homo sapien
15	280.5	18.7	873	2	Q5VVF6_HUMAN	Q5vvf6 homo sapien
16	280	18.6	752	2	Q8NAN7_HUMAN	Q8nan7 homo sapien
17	280	18.6	873	2	Q6S4M1_MACMU	Q6s4m1 macaca mula
18	278.5	18.5	869	2	O42126_XENLA	O42126 xenopus lae
19	277.5	18.5	869	2	Q6NS01_XENLA	Q6ns01 xenopus lae
20	277.5	18.5	904	2	Q5SW65_HUMAN	Q5sw65 homo sapien
21	277.5	18.5	963	1	LRP8_HUMAN	Q14114 homo sapien
22	277.5	18.5	963	2	Q5SW67_HUMAN	Q5sw67 homo sapien
23	277	18.4	845	2	O77505_BOVIN	O77505 bos taurus
24	276.5	18.4	847	2	Q90W12_ONCMY	Q90w12 oncorhynchu
25	275	18.3	845	2	Q91YY0_MOUSE	Q91yy0 mus musculu
26	275	18.3	873	1	VLDLR_MOUSE	P98156 mus musculu
27	271	18.0	844	2	Q6Y857_MORAM	Q6y857 morone amer
28	271	18.0	844	2	Q7ZTG7_OREAU	Q7ztg7 oreochromis
29	271	18.0	873	1	VLDLR_RAT	P98166 rattus norv
30	271	18.0	891	2	Q7YW57_AEDAE	Q7yw57 aedes aegyp
					VLDLR_RABIT	P35953 oryctolagus
32	267	17.8	917	1	LRP8_CHICK	Q98931 gallus gall
33	265	17.6	4260	2	Q4T3T2_TETNG	Q4t3t2 tetraodon n
34	261.5	17.4	1081	2	Q8T4N8_PENSE	Q8t4n8 penaeus sem
35	261	17.4	5141	2	Q700K0_RAT	Q700k0 rattus norv
36	260.5	17.3	173	2	Q5VVF8_HUMAN	Q5vvf8 homo sapien
37	258	17.2	893	2	Q4RJ58_TETNG	Q4rj58 tetraodon n
38	258	17.2	1156	2	Q963T3_AEDAE	Q963t3 aedes aegyp
39	258	17.2	1294	2	Q7QGV0_ANOGA	Q7qgv0 anopheles g
40	255.5	17.0	4660	1	LRP2_RAT	P98158 rattus norv
41	255	17.0	379	2	Q7SXV0_BRARE	Q7sxv0 brachydanio
42	254	16.9	671	2	Q4SEH2_TETNG	Q4seh2 tetraodon n
43	253.5	16.9	1126	2	Q53S76_HUMAN	Q53s76 homo sapien
44	253.5	16.9	1720	2	Q59EV4_HUMAN	Q59ev4 homo sapien
45	253.5	16.9	4599	1	LRP1B_HUMAN	Q9nzr2 homo sapien
46	253	16.8	868	2	Q4SP38_TETNG	Q4sp38 tetraodon n
47	253	16.8	889	2	Q4RUP0_TETNG	Q4rup0 tetraodon n
48	252.5	16.8	891	2	Q7T2X3_CHICK	Q7t2x3 gallus gall
49	252.5	16.8	2304	2	Q4RW33_TETNG	Q4rw33 tetraodon n
50	251.5	16.7	907	2	Q4R1B4_LEUMA	Q4r1b4 leucophaea
51	251	16.7	4544	1	LRP1_HUMAN	Q07954 homo sapien
52	251	16.7	4545	2	Q61291_MOUSE	Q61291 mus musculu
53	251	16.7	4545	2	Q91ZX7_MOUSE	Q91zx7 mus musculu
54	251	16.7	4545	2	Q920Y4_MOUSE	Q920y4 mus musculu
55	250.5	16.7	573	2	Q4T3Z6_TETNG	Q4t3z6 tetraodon n
56	250.5	16.7	4599	1	LRP1B_MOUSE	Q9ji18 mus musculu
57	250	16.6	4071	2	Q6KDZ1_CHICK	Q6kdz1 gallus gall
58	250	16.6	4543	1	LRP1_CHICK	P98157 gallus gall
59	249.5	16.6	4998	2	Q8CG65_MOUSE	Q8cg65 mus musculu
60	249	16.6	591	2	Q6LBN5_HUMAN	Q6lbn5 homo sapien
61	249	16.6	2359	2	Q59FG2_HUMAN	Q59fg2 homo sapien
62	248	16.5	870	2	O02660_BOVIN	O02660 bos taurus
63	248	16.5	5146	2	Q8SPM4_BOVIN	Q8spm4 bos taurus
64	247.5	16.5	1950	1	LRP4_HUMAN	O75096 homo sapien
65	247	16.4	883	2	O46131_LOCMI	O46131 locusta mig
66	245.5	16.3	4753	1	LRP_CAEEL	Q04833 caenorhabd
67	245	16.3	2214	1	SORL_HUMAN	Q92673 h sortilin
68	244	16.2	1984	1	YL_DROME	P98163 drosophila
69	243.5	16.2	1322	2	Q76B61_HUMAN	Q76b61 homo sapie
70	243.5	16.2	4540	2	Q7PS35_ANOGA	Q7ps35 anopheles
71	242.5	16.1	1581	2	O73809_FUGRU	O73809 fugu rubr
72	241	16.0	2215	1	SORL_MOUSE	O88307 m sortili
73	241	16.0	4547	2	Q9W343_DROME	Q9w343 drosophil
74	241	16.0	4655	1	LRP2_HUMAN	P98164 homo sapi
75	241	16.0	4655	2	Q7Z5C0_HUMAN	Q7z5c0 homo sapi
76	241	16.0	4655	2	Q7Z5C1_HUMAN	Q7z5c1 homo sapi
77	240	16.0	773	2	Q53TL0_HUMAN	Q53tl0 homo sap
78	240	16.0	1031	2	Q9VBN0_DROME	Q9vbn0 drosophi
79	240	16.0	1037	2	Q6NP66_DROME	Q6np66 drosophi
80	240	16.0	2378	2	Q4RW31_TETNG	Q4rw31 tetraodo
81	239.5	15.9	3848	2	Q4RG48_TETNG	Q4rg48 tetraodc
82	239	15.9	3881	2	Q4ZG84_HUMAN	Q4zg84 homo sap
83	238.5	15.9	4856	2	Q61EJ2_CAEBR	Q61ej2 caenorha
84	237.5	15.8	820	2	Q96NT6_HUMAN	Q96nt6 homo sap
85	237.5	15.8	862	2	Q53TB8_HUMAN	Q53tb8 homo sap
86	237.5	15.8	1614	1	LRP5_MOUSE	Q91vn0 mus mus
87	237.5	15.8	1639	2	Q571K3_MOUSE	Q571k3 mus mus
88	237.5	15.8	2192	2	O01768_CAEEL	O01768 caenorh
89	237	15.8	1782	2	Q6X0I2_SOLIN	Q6x0i2 solenop
90	236.5	15.7	202	2	Q9NPM0_HUMAN	Q9npm0 homo sa
91	236.5	15.7	316	2	Q4SXP3_TETNG	Q4sxp3 tetrao
92	236	15.7	2213	1	SORL_RABIT	Q95209 o sort
93	235.5	15.7	883	2	Q9VBN1_DROME	Q9vbn1 drosop
94	234.5	15.6	996	2	Q6NP71_DROME	Q6np71 drosop
95	234	15.6	909	2	Q7JP81_CAEEL	Q7jp81 caenor
96	234	15.6	911	2	Q7JP80_CAEEL	Q7jp80 caenor
97	234	15.6	1650	2	Q9QVT6_9MURI	Q9qvt6 rattus
98	234	15.6	2303	2	Q4RXZ9_TETNG	Q4rxz9 tetra
99	233.5	15.5	1252	2	Q9Y0D0_HYDAT	Q9y0d0 hydra
100	233.5	15.5	4699	2	Q9V383_DROME	Q9v383 drosop

ALIGNMENTS

RESULT 3
Q5HZW5_RAT
ID Q5HZW5
AC Q5HZW5
DT 10-MAY-
DT 10-MAY-
DT 10-MAY-
DE Hypothe
GN Name=RGD
OS Rattus n
OC Eukaryot
OC Mammalia
OC Muridae;
OX NCBI_TaxI
RN [1]

insert sequence).
Name=Cd320; Synonyms=425018-1;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
NUCLEOTIDE SEQUENCE.
STRAIN=129;
Rowen L., Qin S., Madan A., Loretz C., Hall J., James R., Dors M.,
Shaffer T., Abbasi N., Ratcliffe A., Dickhoff R., Lasky S., Hood L.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
[2]
NUCLEOTIDE SEQUENCE.
STRAIN=Czech II;
TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
NUCLEOTIDE SEQUENCE.
STRAIN=Czech II;
TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
NIH MGC Project;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
[4]
NUCLEOTIDE SEQUENCE.
STRAIN=129/Sv;
Nagaraja R., Brathwaite M.E., Abe K.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
[5]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
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[6]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brustein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P.A., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
[7]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
The FANTOM Consortium;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
[8]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
[9]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
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sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
[10]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
Adachi J., Aizawa K., Akahira S., Akimura.T., Aono H., Arai A.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,
Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF110520; AAC97969.1; -; Genomic_DNA.
EMBL; BC026888; AAH26888.1; -; mRNA.
EMBL; AF528162; AAO17374.1; -; Genomic_DNA.
EMBL; AK078151; BAC37150.1; -; mRNA.
HSSP; P01130; 1AJJ.
Ensembl; ENSMUSG00000002308; Mus musculus.
MGI; MGI:1860083; Cd320.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR002172; LDL_receptor_A.
Pfam; PF00057; Ldl_recept_a; 2.
PRINTS; PR00261; LDLRECEPTOR.
SMART; SM00192; LDLa; 2.
PROSITE; PS01209; LDLRA_1; 2.
PROSITE; PS50068; LDLRA_2; 2.
Hypothetical protein; Lipoprotein; Receptor.
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Best Local Similarity 57.1%; Pred. No. 3.1e-44;
Matches 160; Conservative 20; Mismatches 75; Indels 25; Gaps 4;

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: May 1, 2006, 17:55:51 ; Search time 46 Seconds
(without alignments)
506.838 Million cell updates/sec

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Perfect score: 1503
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Scoring table: BLOSUM62
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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Qred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1503	100.0	282	2	US-09-907-794A-127	Sequence 127, App
2	1503	100.0	282	2	US-09-905-125A-127	Sequence 127, App
3	1503	100.0	282	2	US-09-902-775A-127	Sequence 127, App
4	1503	100.0	282	2	US-09-906-700-127	Sequence 127, App
5	1503	100.0	282	2	US-09-808-847-1	Sequence 1, Appli
6	1503	100.0	282	2	US-09-903-603A-127	Sequence 127, App
7	1503	100.0	282	2	US-09-904-920A-127	Sequence 127, App
8	1503	100.0	282	2	US-09-909-064-127	Sequence 127, App
9	1503	100.0	282	2	US-09-905-381A-127	Sequence 127, App
10	1503	100.0	282	2	US-09-906-618-127	Sequence 127, App
11	1503	100.0	282	2	US-09-906-646-127	Sequence 127, App
12	1503	100.0	282	2	US-09-904-462-127	Sequence 127, App
13	1503	100.0	282	2	US-09-902-736A-127	Sequence 127, App
14	1503	100.0	282	2	US-09-906-722A-127	Sequence 127, App
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16	342	22.8	132	2	US-09-621-011-147	Sequence 147, App
17	296.5	19.7	904	2	US-09-949-016-9528	Sequence 9528, Ap
18	280	18.6	752	2	US-10-104-047-3003	Sequence 3003, Ap
19	277.5	18.5	873	1	US-08-393-734-2	Sequence 2, Appli
20	277.5	18.5	873	2	US-08-894-489-2	Sequence 2, Appli
21	277.5	18.5	873	2	US-10-167-264-2	Sequence 2, Appli
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23	273.5	18.2	846	1	US-08-451-883-3	Sequence 3, Appli
24	270.5	18.0	846	1	US-08-149-103-4	Sequence 4, Appli
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33	241	16.0	4655	2	US-08-652-877-84	Sequence 84, Appl
34	241	16.0	4655	2	US-08-652-877-86	Sequence 86, Appl
35	241	16.0	4655	2	US-08-652-877-88	Sequence 88, Appl
36	241	16.0	4655	2	US-08-652-877-90	Sequence 90, Appl
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47	226.5	15.1	860	2	US-09-804-778A-8	Sequence 8, Appli
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53	226.5	15.1	1410	1	US-08-470-058-4	Sequence 4, Appli
54	226.5	15.1	1410	2	US-09-037-188-4	Sequence 4, Appli
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56	226.5	15.1	1410	2	US-09-753-385-4	Sequence 4, Appli
57	224.5	14.9	1451	2	US-09-060-299-25	Sequence 25, Appl
58	224.5	14.9	1451	2	US-09-402-923A-25	Sequence 25, Appl
59	224.5	14.9	1584	2	US-09-060-299-39	Sequence 39, Appl
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61	224.5	14.9	1591	2	US-09-060-299-4	Sequence 4, Appli
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73	219.5	14.6	943	2	US-08-476-515A-12	Sequence 12, Appl
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78	205.5	13.7	750	2	US-09-270-767-42975	Sequence 42975, A
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85	194	12.9	713	2	US-10-020-445A-183	Sequence 183, App
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88	188.5	12.5	902	2	US-09-644-600-10	Sequence 10, Appl
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91	183	12.2	302	2	US-09-270-767-33326	Sequence 33326, A
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93	176.5	11.7	136	2	US-09-513-999C-4465	Sequence 4465, Ap
94	173.5	11.5	855	1	US-09-027-337-2	Sequence 2, Appli
95	173.5	11.5	855	2	US-09-644-600-2	Sequence 2, Appli
96	173.5	11.5	855	2	US-09-654-600A-2	Sequence 2, Appli
97	173.5	11.5	855	2	US-10-037-417-132	Sequence 132, App
98	172.5	11.5	242	2	US-09-270-767-32046	Sequence 32046, A
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ALIGNMENTS

RESULT 1
US-09-907-794A-127
; Sequence 127, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
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; ORGANISM: Homo sapiens
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RESULT 2
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; Sequence 127, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: May 1, 2006, 18:08:11 ; Search time 26 Seconds
(without alignments)
493.260 Million cell updates/sec

Title: US-09-904-532B-127
Perfect score: 1503
Sequence: 1 MSGGWMAQVGAWRTGALGLA.....GLLVAMKESLLLSEQKTSLP 282

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep1:*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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6: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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10: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
11: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep1:*
12: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1503	100.0	282	9	US-10-131-826A-312	Sequence 312, App
2	1503	100.0	282	9	US-10-973-115B-312	Sequence 312, App
3	1503	100.0	282	9	US-10-137-873A-312	Sequence 312, App
4	1503	100.0	282	9	US-10-152-370-312	Sequence 312, App
5	1503	100.0	282	11	US-11-080-991-34	Sequence 34, Appl
6	1503	100.0	282	11	US-11-290-153-312	Sequence 312, App
7	280.5	18.7	695	9	US-10-453-372-648	Sequence 648, App
8	280.5	18.7	700	9	US-10-995-561-922	Sequence 922, App
9	280.5	18.7	700	9	US-10-995-561-924	Sequence 924, App
10	280.5	18.7	775	9	US-10-453-372-656	Sequence 656, App
11	280.5	18.7	793	9	US-10-995-561-925	Sequence 925, App
12	280.5	18.7	834	9	US-10-453-372-658	Sequence 658, App
13	280.5	18.7	847	9	US-10-453-372-654	Sequence 654, App
14	280	18.6	752	11	US-11-072-512-3003	Sequence 3003, Ap
15	277.5	18.5	963	9	US-10-995-561-923	Sequence 923, App
16	277.5	18.5	963	9	US-10-453-372-660	Sequence 660, App
17	277.5	18.5	1012	9	US-10-453-372-646	Sequence 646, App
18	267.5	17.8	804	9	US-10-453-372-650	Sequence 650, App
19	267.5	17.8	825	9	US-10-453-372-644	Sequence 644, App
20	258.5	17.2	661	9	US-10-453-372-642	Sequence 642, App
21	251	16.7	4544	9	US-10-501-035-214	Sequence 214, App
22	251	16.7	4544	11	US-11-076-427A-32	Sequence 32, Appl
23	245	16.3	2214	11	US-11-080-991-94	Sequence 94, Appl
24	240	16.0	4655	9	US-10-995-561-556	Sequence 556, App
25	237.5	15.8	1614	11	US-11-108-528-82	Sequence 82, Appl
26	236.5	15.7	857	9	US-10-453-372-652	Sequence 652, App
27	236.5	15.7	905	9	US-10-453-372-638	Sequence 638, App
28	236.5	15.7	905	9	US-10-453-372-662	Sequence 662, App
29	236.5	15.7	905	9	US-10-453-372-664	Sequence 664, App
30	227	15.1	4346	9	US-10-995-561-671	Sequence 671, App
31	227	15.1	4347	9	US-10-995-561-670	Sequence 670, App
32	227	15.1	4390	11	US-11-169-041-169	Sequence 169, App
33	224.5	14.9	1615	11	US-11-108-528-80	Sequence 80, Appl
34	224.5	14.9	1615	11	US-11-124-367A-376	Sequence 376, App
35	224.5	14.9	1627	11	US-11-124-367A-375	Sequence 375, App
36	224.5	14.9	4419	9	US-10-821-234-1155	Sequence 1155, Ap
37	219	14.6	800	11	US-11-217-137-11	Sequence 11, Appl
38	218	14.5	36	9	US-10-957-351-191	Sequence 191, App
39	217	14.4	36	9	US-10-957-351-190	Sequence 190, App
40	216	14.4	1113	11	US-11-067-811-4	Sequence 4, Appli
41	214	14.2	1613	11	US-11-108-528-84	Sequence 84, Appl
42	214	14.2	1613	11	US-11-108-528-86	Sequence 86, Appl
43	202.5	13.5	336	9	US-10-453-372-640	Sequence 640, App
44	201	13.4	1042	11	US-11-067-811-1	Sequence 1, Appli
45	194	12.9	419	9	US-10-821-234-1556	Sequence 1556, Ap
46	194	12.9	713	9	US-10-194-487-416	Sequence 416, App
47	194	12.9	713	9	US-10-195-883-416	Sequence 416, App
48	194	12.9	713	9	US-10-195-888-416	Sequence 416, App
49	194	12.9	713	9	US-10-195-889-416	Sequence 416, App
50	194	12.9	713	9	US-10-216-161A-183	Sequence 183, App
51	191	12.7	234	11	US-11-124-367A-470	Sequence 470, App
52	187.5	12.5	850	11	US-11-037-243-108	Sequence 108, App
53	186	12.4	1678	11	US-11-124-367A-340	Sequence 340, App
54	186	12.4	1678	11	US-11-124-367A-341	Sequence 341, App
55	182	12.1	1115	9	US-10-055-877-160	Sequence 160, App
56	173.5	11.5	855	11	US-11-104-110-1	Sequence 1, Appli
57	173.5	11.5	855	11	US-11-019-711-132	Sequence 132, App
58	173.5	11.5	855	11	US-11-104-111-22	Sequence 22, Appl
59	166	11.0	802	9	US-10-216-161A-169	Sequence 169, App
60	166	11.0	802	11	US-11-037-243-113	Sequence 113, App
61	162.5	10.8	859	11	US-11-000-463-423	Sequence 423, App
62	162.5	10.8	859	11	US-11-000-463-895	Sequence 895, App
63	160.5	10.7	435	11	US-11-077-386-19	Sequence 19, Appl
64	160.5	10.7	450	11	US-11-077-386-20	Sequence 20, Appl
65	158.5	10.5	399	11	US-11-077-386-18	Sequence 18, Appl
66	141	9.4	36	9	US-10-957-351-86	Sequence 86, Appl
67	140.5	9.3	277	11	US-11-132-285-3	Sequence 3, Appli
68	140.5	9.3	277	11	US-11-182-946-12	Sequence 12, Appl
69	140.5	9.3	652	9	US-10-821-234-1016	Sequence 1016, Ap
70	137.5	9.1	51	9	US-10-957-351-353	Sequence 353, App
71	135.5	9.0	35	9	US-10-957-351-106	Sequence 106, App
72	130	8.6	40	9	US-10-957-351-352	Sequence 352, App
73	129.5	8.6	35	9	US-10-957-351-71	Sequence 71, Appl
74	125	8.3	737	9	US-10-194-487-38	Sequence 38, Appl
75	125	8.3	737	9	US-10-195-883-38	Sequence 38, Appl
76	125	8.3	737	9	US-10-195-888-38	Sequence 38, Appl
77	125	8.3	737	9	US-10-195-889-38	Sequence 38, Appl
78	123	8.2	37	9	US-10-957-351-8	Sequence 8, Appli
79	122.5	8.2	427	11	US-11-182-946-5	Sequence 5, Appli
80	122.5	8.2	427	11	US-11-185-878-4	Sequence 4, Appli
81	122	8.1	36	9	US-10-957-351-153	Sequence 153, App
82	121	8.1	38	9	US-10-957-351-103	Sequence 103, App
83	121	8.1	383	9	US-10-242-586-80	Sequence 80, Appl
84	121	8.1	383	9	US-10-242-902-80	Sequence 80, Appl
85	121	8.1	383	9	US-10-243-116-80	Sequence 80, Appl
86	121	8.1	383	9	US-10-243-136-80	Sequence 80, Appl
87	121	8.1	383	9	US-10-243-189-80	Sequence 80, Appl
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91	121	8.1	383	9	US-10-243-304-80	Sequence 80, Appl
92	121	8.1	383	9	US-10-243-338-80	Sequence 80, Appl
93	121	8.1	383	9	US-10-243-345-80	Sequence 80, Appl
94	121	8.1	383	9	US-10-243-357-80	Sequence 80, Appl

95	121	8.1	383	9	US-10-245-083-80	Sequence 80, Appl
96	121	8.1	383	9	US-10-247-015-80	Sequence 80, Appl
97	121	8.1	383	11	US-11-147-047-38	Sequence 38, Appl
98	121	8.1	383	11	US-11-264-096-770	Sequence 770, App
99	120.5	8.0	969	9	US-10-055-877-214	Sequence 214, App
100	120	8.0	401	11	US-11-072-175-224	Sequence 224, App

ALIGNMENTS

RESULT 1
US-10-131-826A-312
; Sequence 312, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 312
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-312

Query Match 100.0%; Score 1503; DB 9; Length 282;
Best Local Similarity 100.0%; Pred. No. 3.4e-108;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 CRTSGLCVPLTWRCDRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGT 120
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RESULT 2
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; Sequence 312, Application US/10973115B
; Publication No. US20060040351A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Quiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCC
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 39870-3330R1C300C1
; CURRENT APPLICATION NUMBER: US/10/973,115B
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 10/145,747
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 10/028,072
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/581,742
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/05746
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/135,736
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/123,090
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 312
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-973-115B-312

Query Match 100.0%; Score 1503; DB 9; Length 282;
Best Local Similarity 100.0%; Pred. No. 3.4e-108;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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